



## wwPDB EM Validation Summary Report ⓘ

Mar 25, 2026 – 11:24 AM UTC

PDB ID : 2J28 / pdb\_00002j28  
EMDB ID : EMD-1261  
Title : MODEL OF E. COLI SRP BOUND TO 70S RNCS  
Authors : Halic, M.; Blau, M.; Becker, T.; Mielke, T.; Pool, M.R.; Wild, K.; Sinning, I.; Beckmann, R.  
Deposited on : 2006-08-16  
Resolution : 9.50 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

EMDB validation analysis : 0.0.1.dev132  
MolProbity : 4-5-2 with Phenix2.0  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.49

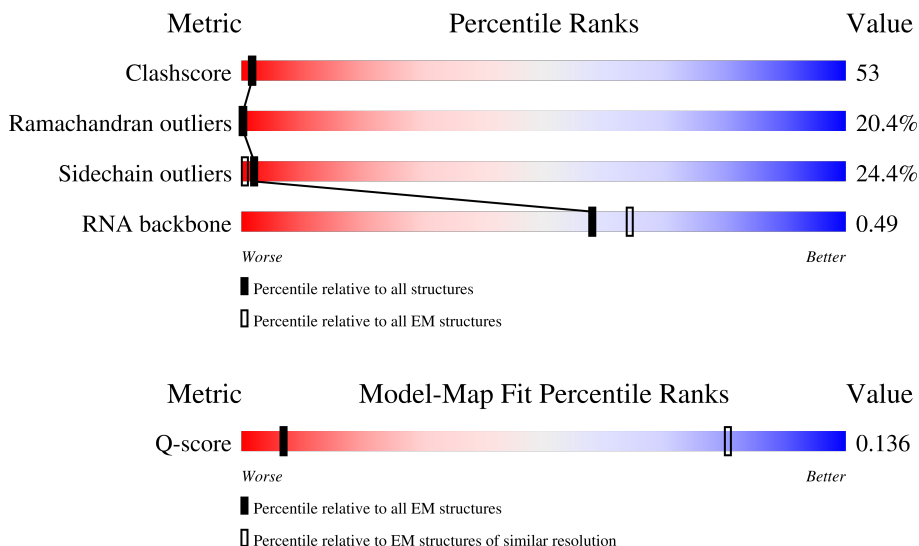
# 1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 9.50 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	234 ( 9.00 - 10.00 )

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion  $< 40\%$ ). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	0	56	<div style="display: flex; justify-content: space-between; align-items: center;"> <div style="text-align: center;"> <p>39%</p> <p>11%</p> </div> <div style="text-align: center;"> <p>48%</p> </div> <div style="text-align: center;"> <p>32%</p> </div> <div style="text-align: center;"> <p>9%</p> </div> </div>
2	1	54	<div style="display: flex; justify-content: space-between; align-items: center;"> <div style="text-align: center;"> <p>33%</p> <p>20%</p> </div> <div style="text-align: center;"> <p>43%</p> </div> <div style="text-align: center;"> <p>35%</p> </div> <div style="text-align: center;"> <p>•</p> </div> </div>
3	2	46	<div style="display: flex; justify-content: space-between; align-items: center;"> <div style="text-align: center;"> <p>52%</p> <p>26%</p> </div> <div style="text-align: center;"> <p>48%</p> </div> <div style="text-align: center;"> <p>15%</p> </div> <div style="text-align: center;"> <p>11%</p> </div> </div>

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Mol	Chain	Length	Quality of chain
4	3	64	52% 25% 45% 27%
5	4	38	45% 5% 47% 24% 24%
6	7	18	22% 17% 72% 11%
7	8	74	5% 73% 19% 5%
8	9	430	76% 42% 45% 10%
9	A	117	26% 62% 12%
10	B	2904	27% 58% 12%
11	C	267	41% 12% 42% 36% 10%
12	D	209	21% 18% 42% 34% 6%
13	E	201	33% 18% 45% 31% 6%
14	F	178	8% 20% 47% 26% 7%
15	G	176	6% 30% 52% 16%
16	H	149	74% 20% 58% 17% 5%
17	I	141	36% 30% 62% 8%
18	J	140	28% 12% 49% 34%
19	K	121	19% 15% 44% 36% 5%
20	L	144	33% 15% 37% 29% 19%
21	M	136	32% 17% 43% 29% 10%
22	N	127	24% 21% 54% 22%
23	O	117	9% 18% 61% 18%
24	P	114	33% 10% 35% 32% 24%
25	Q	117	25% 19% 55% 21% 6%
26	R	103	24% 17% 37% 35% 11%
27	S	110	32% 21% 52% 25%
28	T	99	32% 13% 48% 33% 5%

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Mol	Chain	Length	Quality of chain
29	U	102	
30	V	94	
31	W	84	
32	X	63	
33	Y	58	
34	Z	70	

## 2 Entry composition

There are 36 unique types of molecules in this entry. The entry contains 95358 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	0	56	444	269	94	80	1	0	0

- Molecule 2 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
2	1	54	441	284	81	76	0	0

- Molecule 3 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	2	46	377	228	90	57	2	0	0

- Molecule 4 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	3	64	504	323	105	74	2	0	0

- Molecule 5 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	4	38	302	185	65	48	4	0	0

- Molecule 6 is a protein called SIGNAL SEQUENCE.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
6	7	18	149	103	23	23	0	0

- Molecule 7 is a RNA chain called 4.5S SIGNAL RECOGNITION PARTICLE RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	8	74	Total	C	N	O	P	0	0
			1590	709	295	512	74		

- Molecule 8 is a protein called Signal recognition particle protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	9	430	Total	C	N	O	S	0	0
			3306	2072	595	617	22		

- Molecule 9 is a RNA chain called 5S RIBOSOMAL RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	A	117	Total	C	N	O	P	0	0
			2507	1116	459	815	117		

- Molecule 10 is a RNA chain called 23S RIBOSOMAL RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	B	2841	Total	C	N	O	P	0	0
			60995	27210	11229	19715	2841		

- Molecule 11 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	C	267	Total	C	N	O	S	0	0
			2053	1271	416	359	7		

- Molecule 12 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	D	209	Total	C	N	O	S	0	0
			1565	979	288	294	4		

- Molecule 13 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	E	201	Total	C	N	O	S	0	0
			1552	974	283	290	5		

- Molecule 14 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
14	F	178	1420	905	251	258	6	0	0

- Molecule 15 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
15	G	176	1323	832	243	246	2	0	0

- Molecule 16 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
16	H	149	1111	699	197	214	1	0	0

- Molecule 17 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
17	I	141	1032	651	179	196	6	0	0

- Molecule 18 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
18	J	140	1112	704	210	194	4	0	0

- Molecule 19 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
19	K	121	930	582	179	164	5	0	0

- Molecule 20 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
20	L	144	1053	654	207	190	2	0	0

- Molecule 21 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	M	136	Total	C	N	O	S	0	0
			1074	686	205	177	6		

- Molecule 22 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	N	127	Total	C	N	O	S	0	0
			1008	621	204	178	5		

- Molecule 23 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	O	117	Total	C	N	O	S	0	0
			900	557	179	163	1		

- Molecule 24 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	P	114	Total	C	N	O	S	0	0
			917	574	179	163	1		

- Molecule 25 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms				AltConf	Trace
25	Q	117	Total	C	N	O	0	0
			947	604	192	151		

- Molecule 26 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	R	103	Total	C	N	O	S	0	0
			816	516	153	145	2		

- Molecule 27 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	S	110	Total	C	N	O	S	0	0
			857	532	166	156	3		

- Molecule 28 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
28	T	99	777	491	145	139	2	0	0

- Molecule 29 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
29	U	102	779	492	146	141		0	0

- Molecule 30 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
30	V	94	753	479	137	134	3	0	0

- Molecule 31 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
31	W	84	634	391	129	113	1	0	0

- Molecule 32 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
32	X	63	509	313	99	95	2	0	0

- Molecule 33 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
33	Y	58	449	281	87	79	2	0	0

- Molecule 34 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
34	Z	70	549	339	104	100	6	0	0

- Molecule 35 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
35	B	110	Total 110	Mg 110	0
35	N	1	Total 1	Mg 1	0

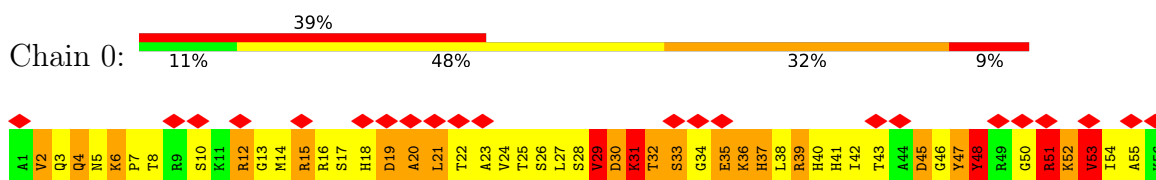
- Molecule 36 is water.

Mol	Chain	Residues	Atoms		AltConf
36	B	506	Total 506	O 506	0
36	N	6	Total 6	O 6	0

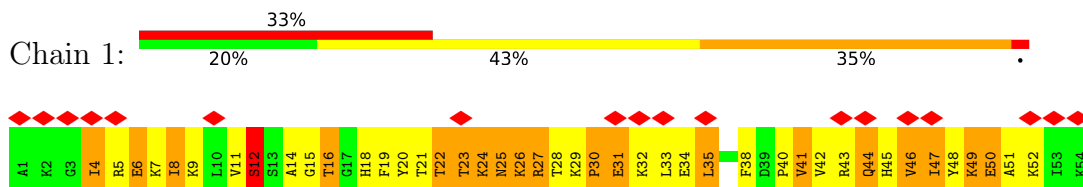
### 3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

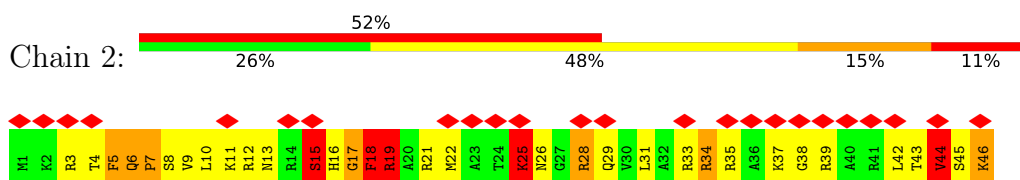
- Molecule 1: 50S ribosomal protein L32



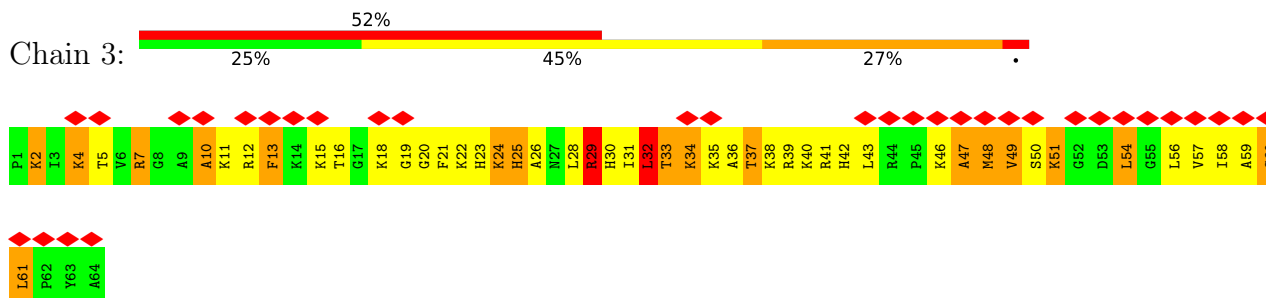
- Molecule 2: 50S ribosomal protein L33



- Molecule 3: 50S ribosomal protein L34

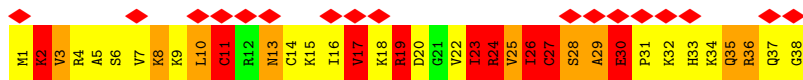


- Molecule 4: 50S ribosomal protein L35



- Molecule 5: 50S ribosomal protein L36

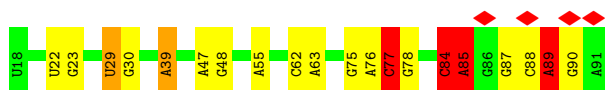




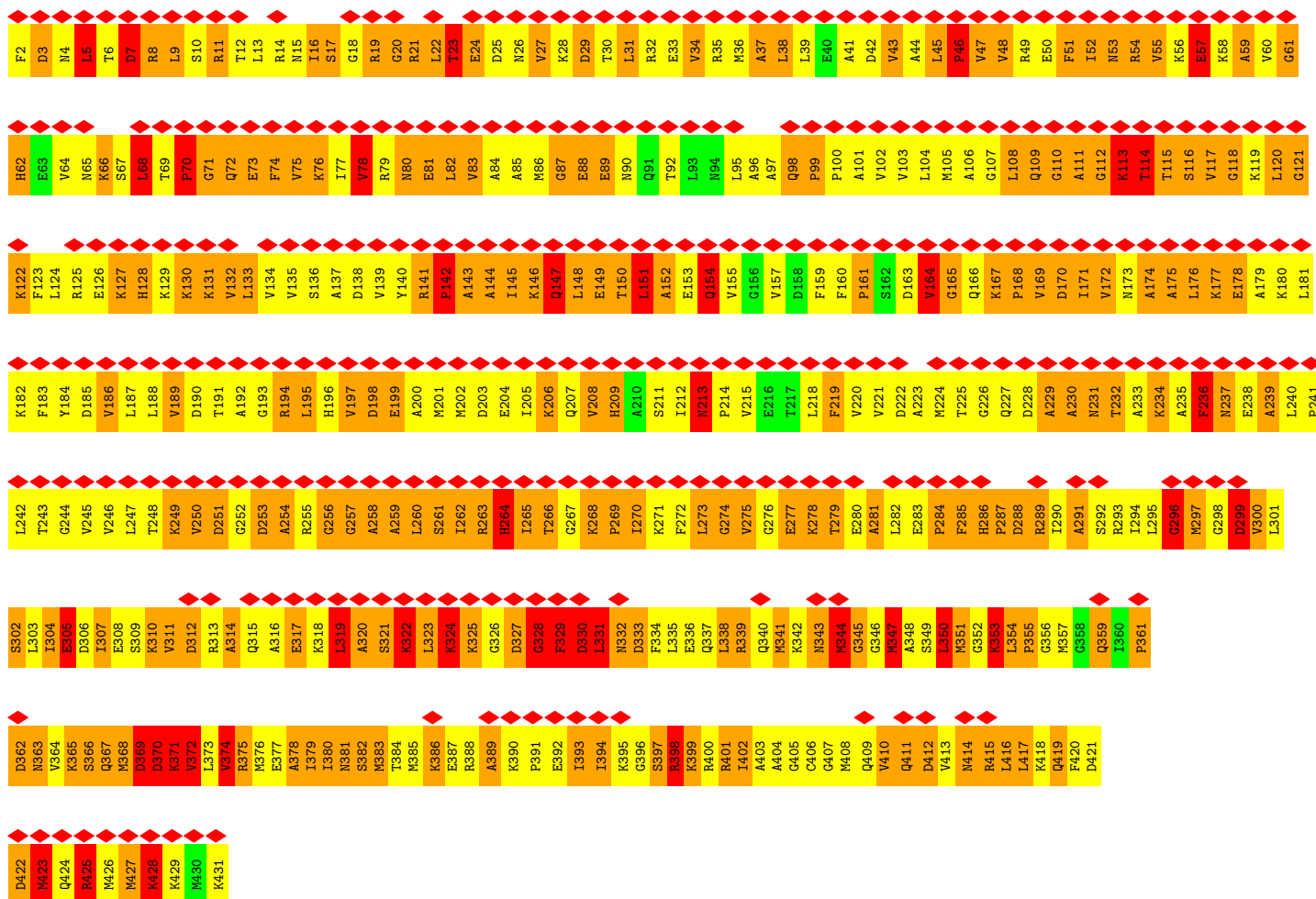
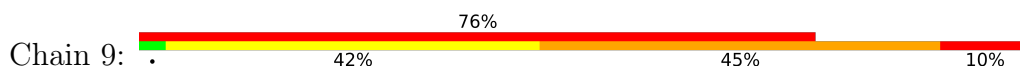
• Molecule 6: SIGNAL SEQUENCE



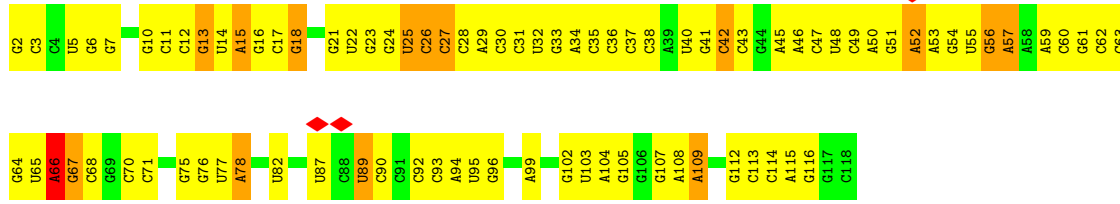
• Molecule 7: 4.5S SIGNAL RECOGNITION PARTICLE RNA



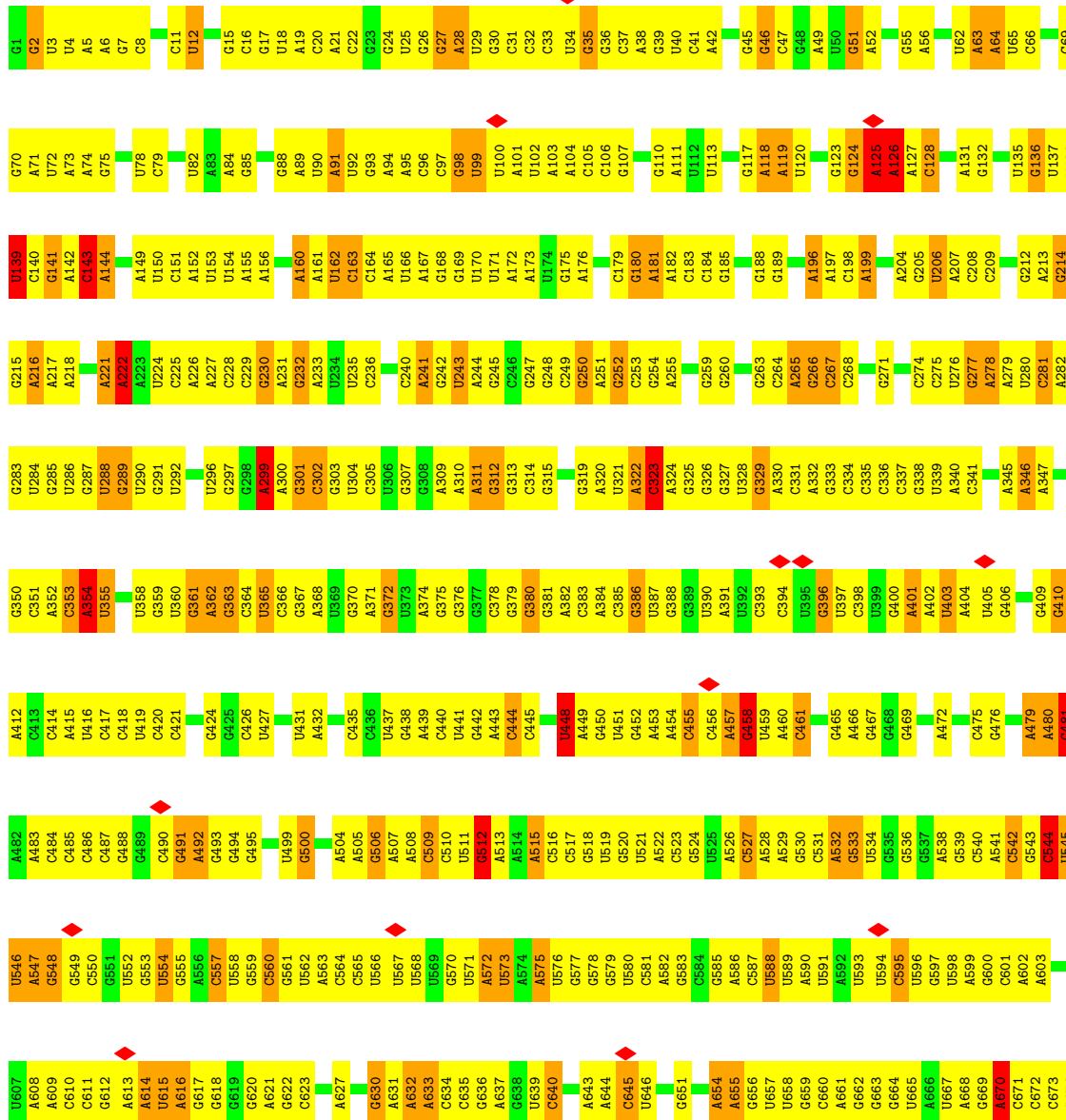
• Molecule 8: Signal recognition particle protein



• Molecule 9: 5S RIBOSOMAL RNA

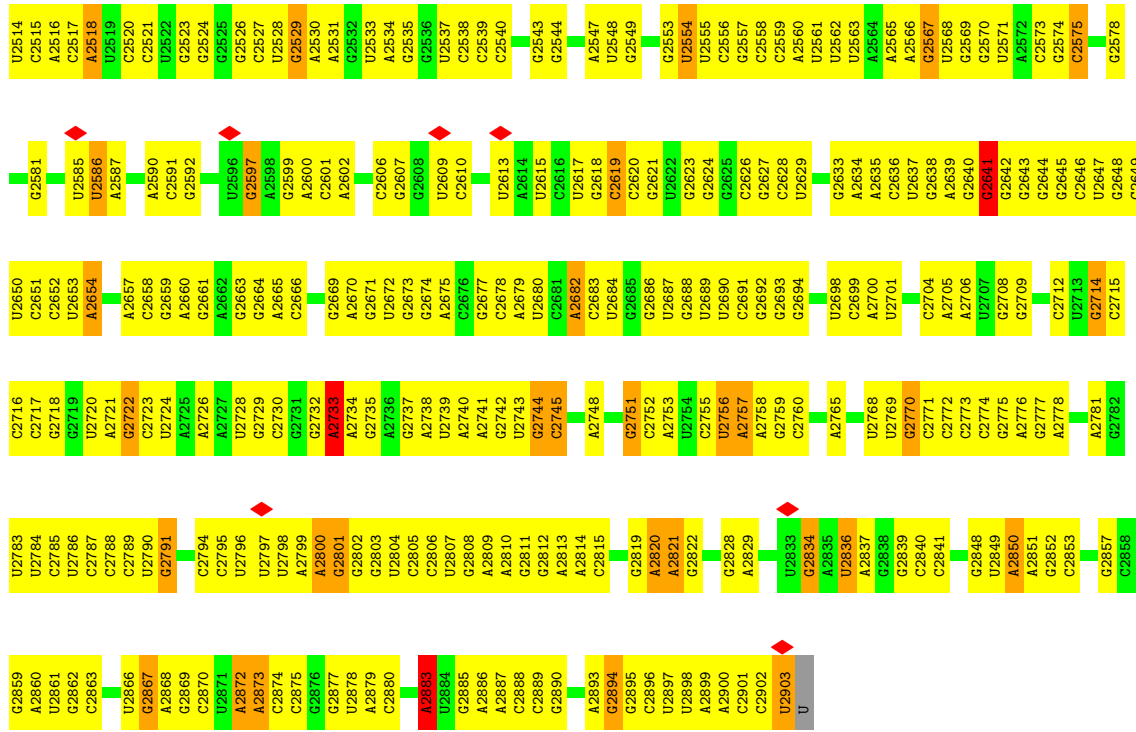


• Molecule 10: 23S RIBOSOMAL RNA

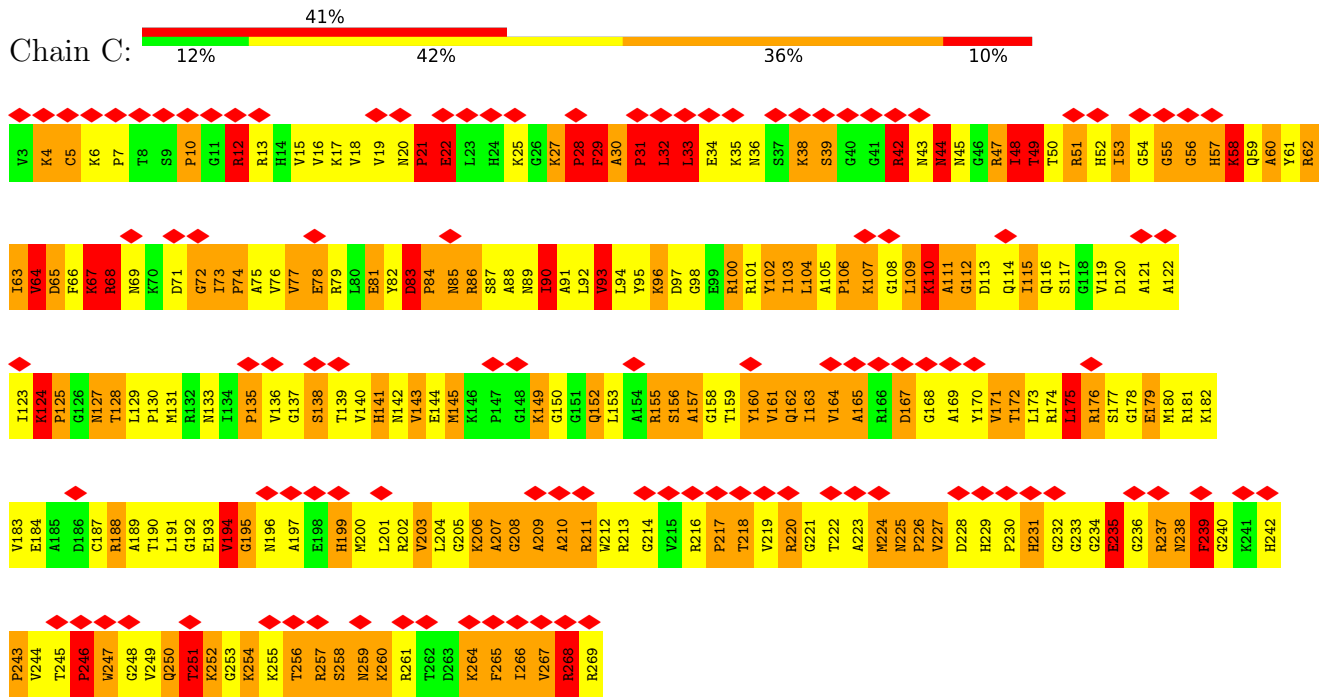


A1505	A1506	A1507	A1508	A1509	G1510	G1511	G1512	G1513	G1514	G1515	G1516	G1517	G1518	G1519	G1520	G1521	G1522	G1523	G1524	G1525	G1526	G1527	G1528	G1529	G1530	G1531	G1532	G1533	G1534	G1535	G1536	G1537	G1538	G1539	G1540	G1541	G1542	G1543	G1544	G1545	G1546	G1547	G1548	G1549	G1550	G1551	G1552	G1553	G1554	G1555	G1556	G1557	G1558	G1559	G1560	G1561	G1562	G1563	G1564	G1565	G1566	G1567	G1642																							
A1434	A1435	A1436	A1437	A1438	A1439	A1440	A1441	A1442	A1443	A1444	A1445	A1446	A1447	A1448	A1449	A1450	A1451	A1452	A1453	A1454	A1455	A1456	A1457	A1458	A1459	A1460	A1461	A1462	A1463	A1464	A1465	A1466	A1467	A1468	A1469	A1470	A1471	A1472	A1473	A1474	A1475	A1476	A1477	A1478	A1479	A1480	A1481	A1482	A1483	A1484	A1485	A1486	A1487	A1488	A1489	A1490	A1491	A1492	A1493	A1494	A1495	A1496	A1504																							
C1362	C1363	C1364	C1365	C1366	C1367	C1368	C1369	C1370	C1371	C1372	C1373	C1374	C1375	C1376	C1377	C1378	C1379	C1380	C1381	C1382	C1383	C1384	C1385	C1386	C1387	C1388	C1389	C1390	C1391	C1392	C1393	C1394	C1395	C1396	C1397	C1398	C1399	C1400	C1401	C1402	C1403	C1404	C1405	C1406	C1407	C1408	C1409	C1410	C1411	C1412	C1413	C1414	C1415	C1416	C1417	C1418	C1419	C1420	C1421	C1422	C1423	C1424	C1425	C1426	C1427	C1428	C1429	C1430	C1431	C1432	C1433															
C1295	C1296	C1297	C1298	C1299	C1300	C1301	C1302	C1303	C1304	C1305	C1306	C1307	C1308	C1309	C1310	C1311	C1312	C1313	C1314	C1315	C1316	C1317	C1318	C1319	C1320	C1321	C1322	C1323	C1324	C1325	C1326	C1327	C1328	C1329	C1330	C1331	C1332	C1333	C1334	C1335	C1336	C1337	C1338	C1339	C1340	C1341	C1342	C1343	C1344	C1345	C1346	C1347	C1348	C1349	C1350	C1351	C1352	C1353	C1354	C1355	C1356	C1357	C1358	C1359	C1360	C1361																				
G1235	G1236	G1237	G1238	G1239	G1240	G1241	G1242	G1243	G1244	G1245	G1246	G1247	G1248	G1249	G1250	G1251	G1252	G1253	G1254	G1255	G1256	G1257	G1258	G1259	G1260	G1261	G1262	G1263	G1264	G1265	G1266	G1267	G1268	G1269	G1270	G1271	G1272	G1273	G1274	G1275	G1276	G1277	G1278	G1279	G1280	G1281	G1282	G1283	G1284	G1285	G1286	G1287	G1288	G1289	G1290	G1291	G1292	G1293	G1294																											
U1101	U1102	U1103	U1104	U1105	U1106	U1107	U1108	U1109	U1110	U1111	U1112	U1113	U1114	U1115	U1116	U1117	U1118	U1119	U1120	U1121	U1122	U1123	U1124	U1125	U1126	U1127	U1128	U1129	U1130	U1131	U1132	U1133	U1134	U1135	U1136	U1137	U1138	U1139	U1140	U1141	U1142	U1143	U1144	U1145	U1146	U1147	U1148	U1149	U1150	U1151	U1152	U1153	U1154	U1155	U1156	U1157	U1158	U1159	U1160	U1161	U1162	U1163	U1164	U1165	U1166																					
C1157	C1158	C1159	C1160	C1161	C1162	C1163	C1164	C1165	C1166	C1167	C1168	C1169	C1170	C1171	C1172	C1173	C1174	C1175	C1176	C1177	C1178	C1179	C1180	C1181	C1182	C1183	C1184	C1185	C1186	C1187	C1188	C1189	C1190	C1191	C1192	C1193	C1194	C1195	C1196	C1197	C1198	C1199	C1200	C1201	C1202	C1203	C1204	C1205	C1206	C1207	C1208	C1209	C1210	C1211	C1212	C1213	C1214	C1215	C1216	C1217	C1218	C1219	C1220	C1221	C1222	C1223	C1224	C1225	C1226	C1227	C1228	C1229	C1230													
G1024	G1025	G1026	G1027	G1028	G1029	G1030	G1031	G1032	G1033	G1034	G1035	G1036	G1037	G1038	G1039	G1040	G1041	G1042	G1043	G1044	G1045	G1046	G1047	G1048	G1049	G1050	G1051	G1052	G1053	G1054	G1055	G1056	G1057	G1058	G1059	G1060	G1061	G1062	G1063	G1064	G1065	G1066	G1067	G1068	G1069	G1070	G1071	G1072	G1073	G1074	G1075	G1076	G1077	G1078	G1079	G1080	G1081	G1082	G1083	G1084	G1085	G1086	G1087	G1088	G1089	G1090	G1091	G1092	G1093	G1094	G1095	G1096	G1097	G1098	G1099	G1100										
U986	U987	U988	U989	U990	U991	U992	U993	U994	U995	U996	U997	U998	U999	U1000	U1001	U1002	U1003	U1004	U1005	U1006	U1007	U1008	U1009	U1010	U1011	U1012	U1013	U1014	U1015	U1016	U1017	U1018	U1019	U1020	U1021	U1022	U1023	U1024	U1025	U1026	U1027	U1028	U1029	U1030	U1031	U1032	U1033	U1034	U1035	U1036	U1037	U1038	U1039	U1040	U1041	U1042	U1043	U1044	U1045	U1046	U1047	U1048	U1049	U1050	U1051	U1052	U1053	U1054	U1055	U1056	U1057	U1058	U1059	U1060												
C836	C837	C838	C839	C840	C841	C842	C843	C844	C845	C846	C847	C848	C849	C850	C851	C852	C853	C854	C855	C856	C857	C858	C859	C860	C861	C862	C863	C864	C865	C866	C867	C868	C869	C870	C871	C872	C873	C874	C875	C876	C877	C878	C879	C880	C881	C882	C883	C884	C885	C886	C887	C888	C889	C890	C891	C892	C893	C894	C895	C896	C897	C898	C899	C900	C901	C902	C903	C904	C905	C906	C907	C908	C909	C910	C911	C912	C913	C914	C915	C916	C917	C918	C919	C920	C921	C922
G836	G837	G838	G839	G840	G841	G842	G843	G844	G845	G846	G847	G848	G849	G850	G851	G852	G853	G854	G855	G856	G857	G858	G859	G860	G861	G862	G863	G864	G865	G866	G867	G868	G869	G870	G871	G872	G873	G874	G875	G876	G877	G878	G879	G880	G881	G882	G883	G884	G885	G886	G887	G888	G889	G890	G891	G892	G893	G894	G895	G896	G897	G898	G899	G900	G901	G902	G903	G904	G905	G906	G907	G908	G909	G910	G911	G912	G913	G914	G915	G916	G917	G918	G919	G920	G921	G922
C757	C758	C759	C760	C761	C762	C763	C764	C765	C766	C767	C768	C769	C770	C771	C772	C773	C774	C775	C776	C777	C778	C779	C780	C781	C782	C783	C784	C785	C786	C787	C788	C789	C790	C791	C792	C793	C794	C795	C796	C797	C798	C799	C800	C801	C802	C803	C804	C805	C806	C807	C808	C809	C810	C811	C812	C813	C814	C815	C816	C817	C818	C819	C820	C821	C822	C823	C824	C825	C826	C827	C828	C829	C830	C831	C832	C833	C834	C835								
A675	A676	A677	A678	A679	A680	A681	A682	A683	A684	A685	A686	A687	A688	A689	A690	A691	A692	A693	A694	A695	A696	A697	A698	A699	A700	A701	A702	A703	A704	A705	A706	A707	A708	A709	A710	A711	A712	A713	A714	A715	A716	A717	A718	A719	A720	A721	A722	A723	A724	A725	A726	A727	A728	A729	A730	A731	A732	A733	A734	A735	A736	A737	A738	A739	A740	A741	A742	A743	A744	A745	A746	A747	A748	A749	A750	A751	A752	A753	A754	A755	A756					

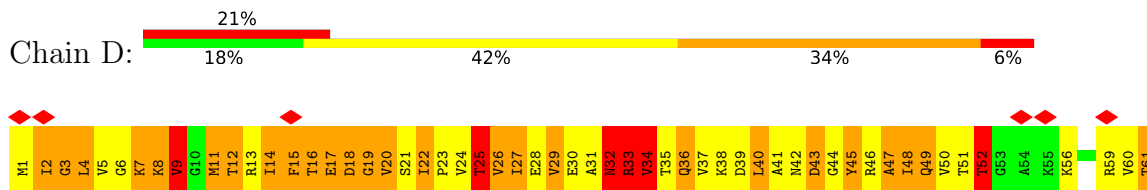


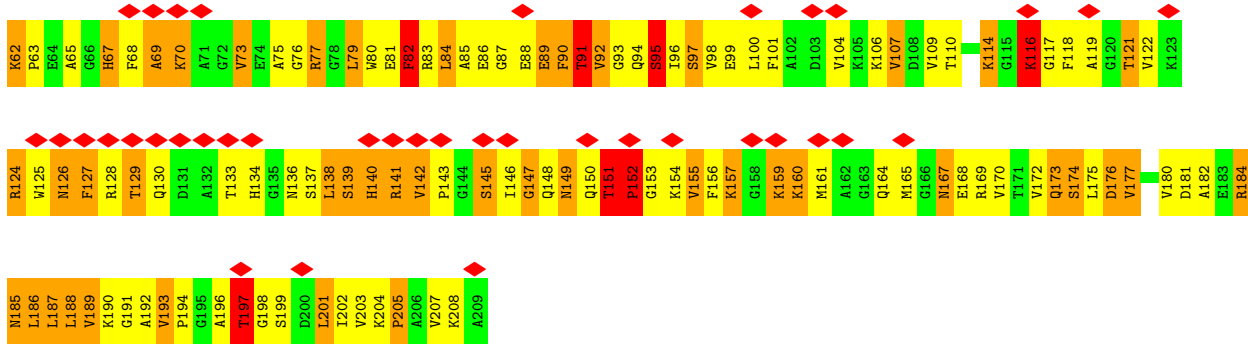


• Molecule 11: 50S ribosomal protein L2

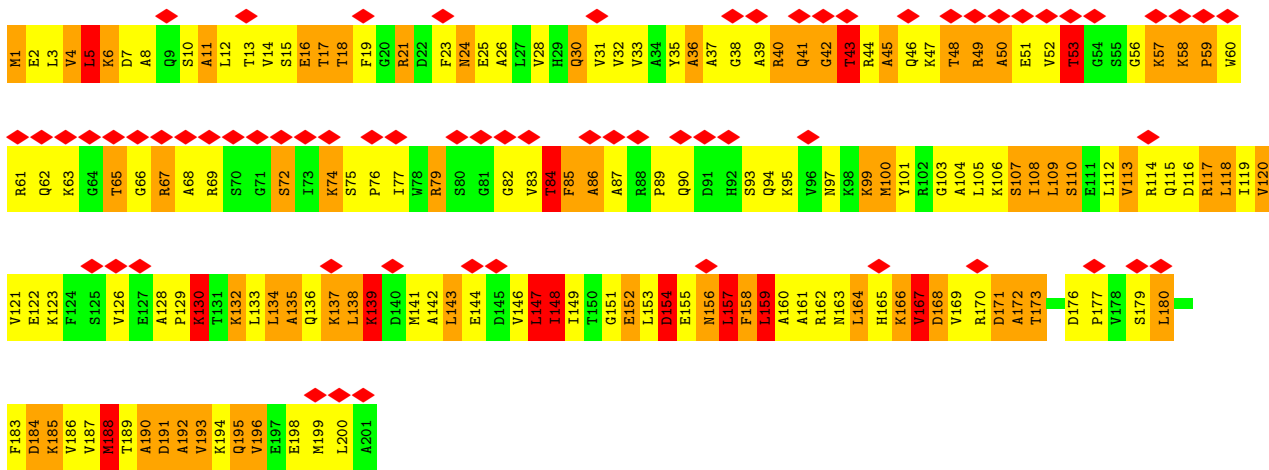
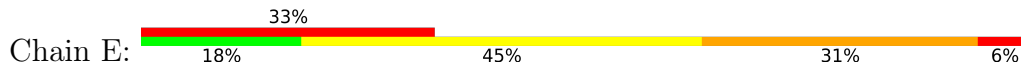


• Molecule 12: 50S ribosomal protein L3

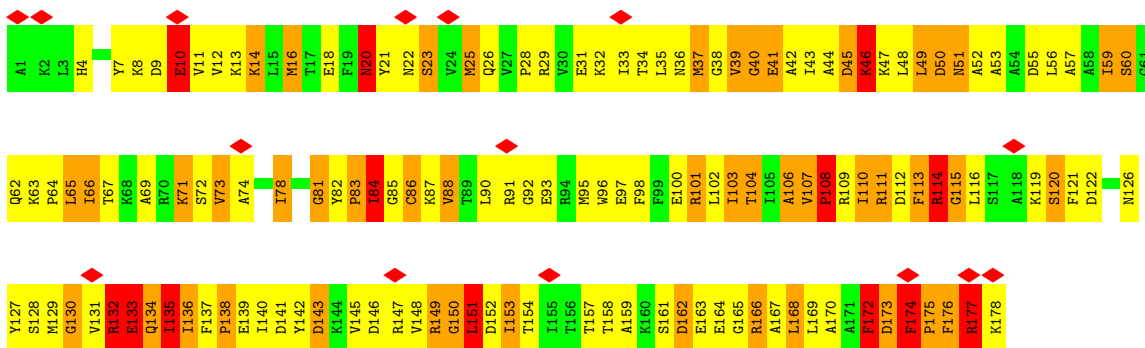
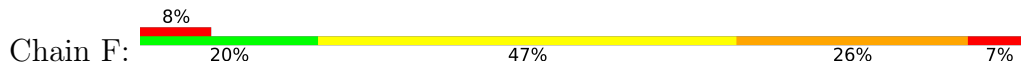




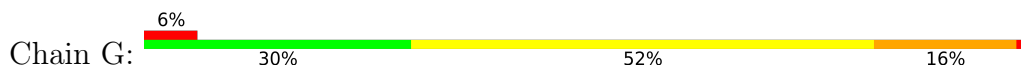
• Molecule 13: 50S ribosomal protein L4

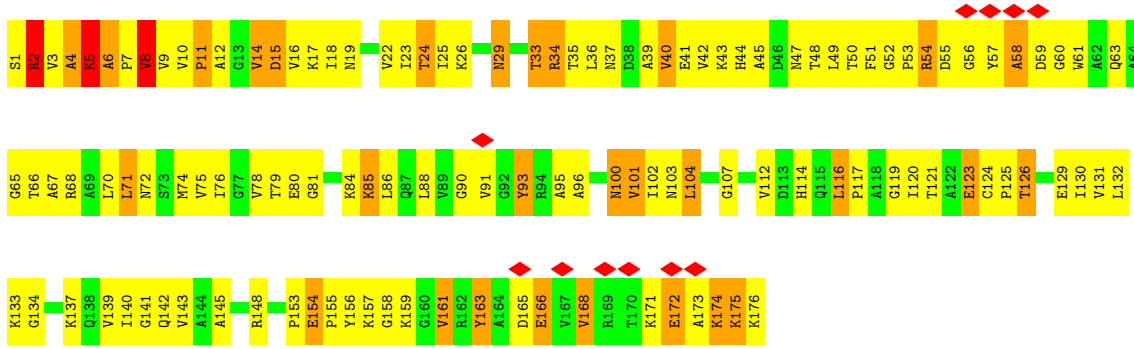


• Molecule 14: 50S ribosomal protein L5

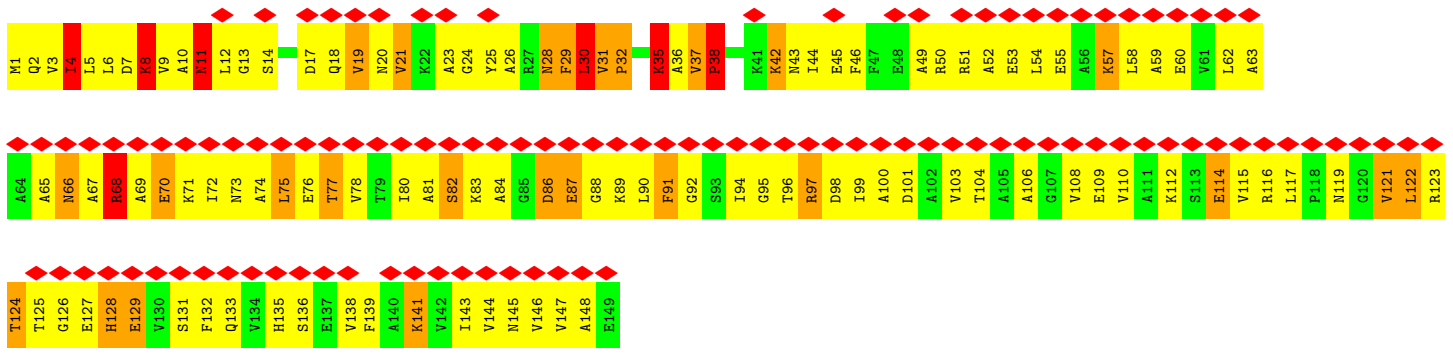
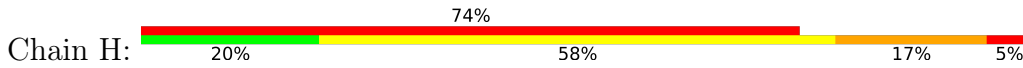


• Molecule 15: 50S ribosomal protein L6

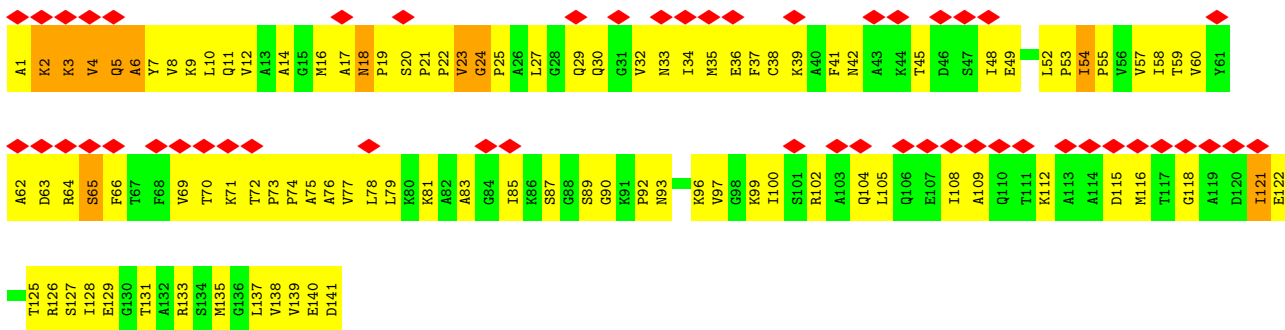




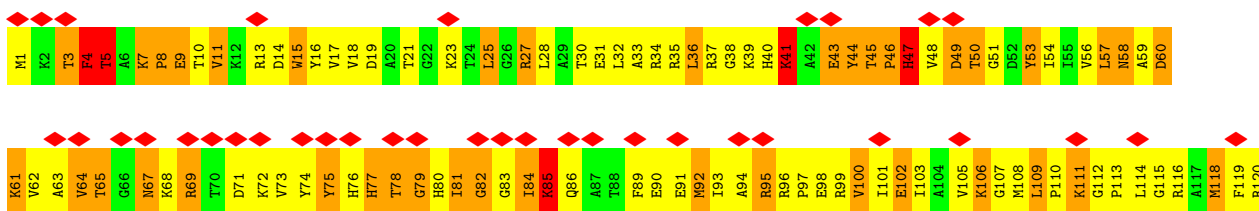
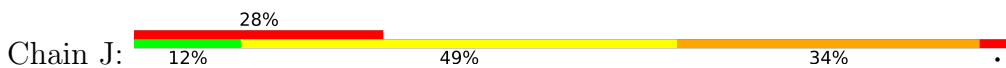
• Molecule 16: 50S ribosomal protein L9



• Molecule 17: 50S ribosomal protein L11

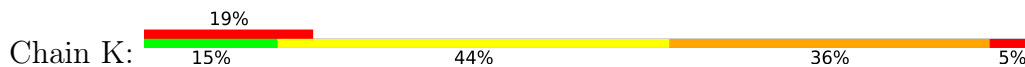


• Molecule 18: 50S ribosomal protein L13

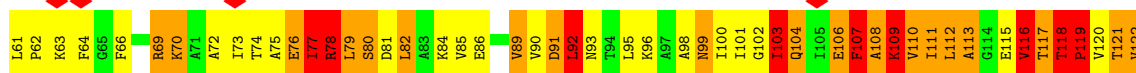




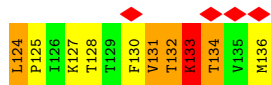
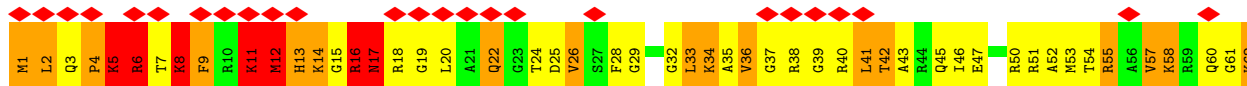
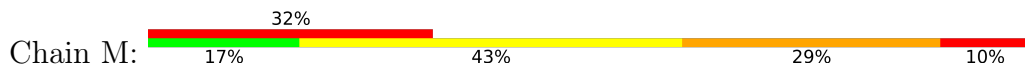
• Molecule 19: 50S ribosomal protein L14



• Molecule 20: 50S ribosomal protein L15

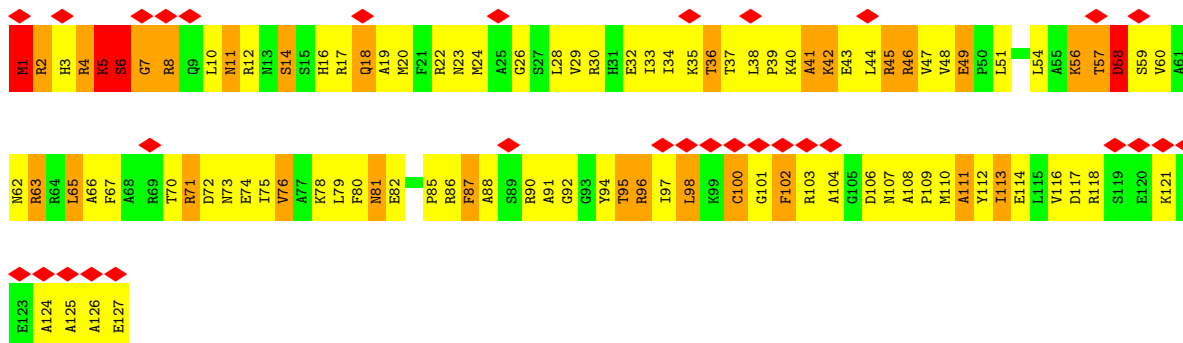


• Molecule 21: 50S ribosomal protein L16

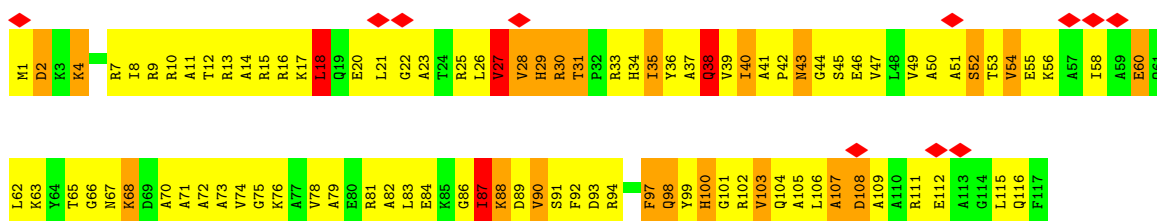


• Molecule 22: 50S ribosomal protein L17

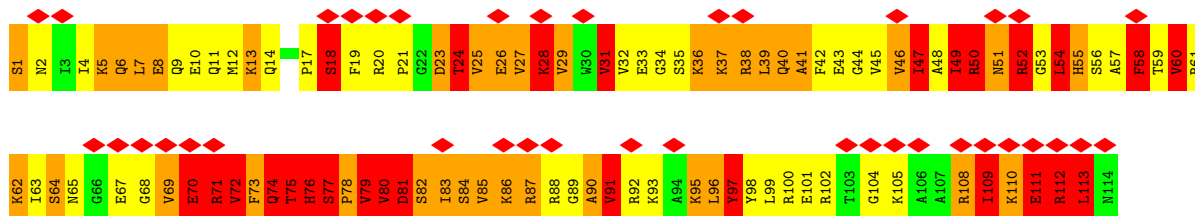




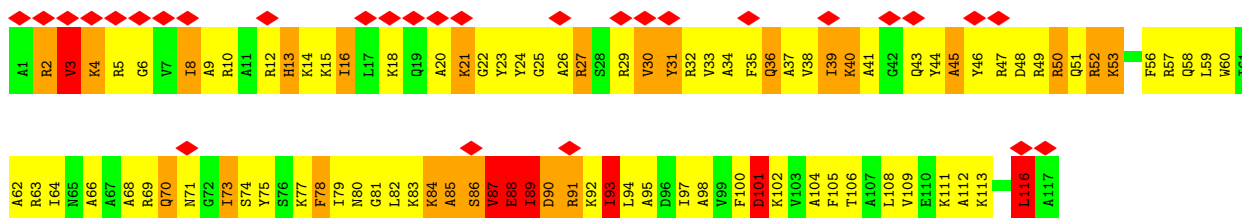
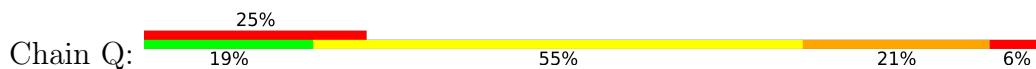
• Molecule 23: 50S ribosomal protein L18



• Molecule 24: 50S ribosomal protein L19

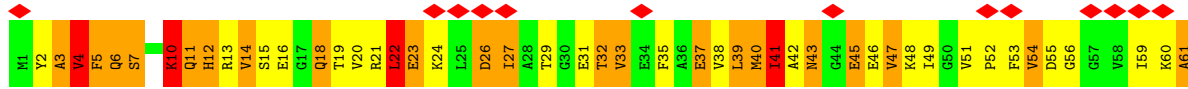


• Molecule 25: 50S ribosomal protein L20

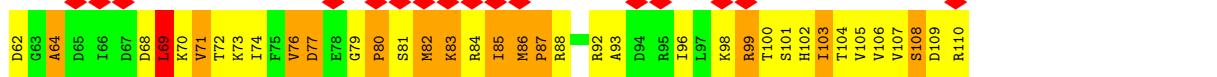
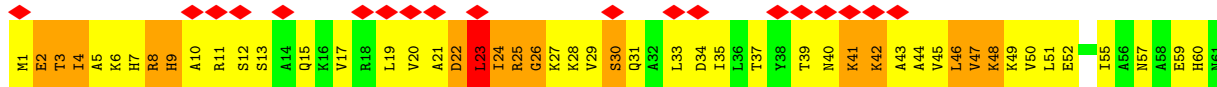
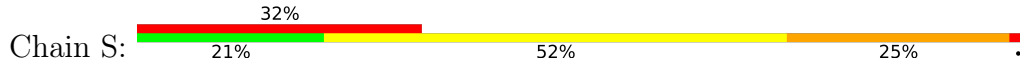


• Molecule 26: 50S ribosomal protein L21

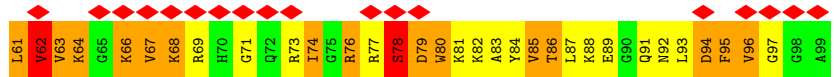
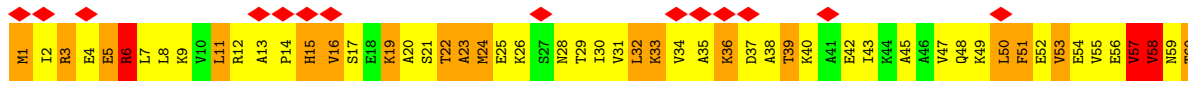
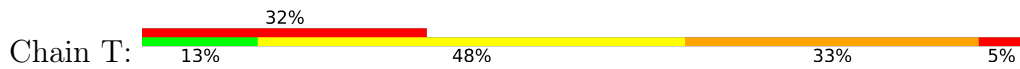




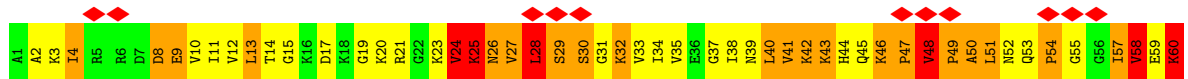
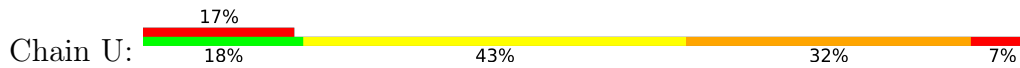
• Molecule 27: 50S ribosomal protein L22



• Molecule 28: 50S ribosomal protein L23



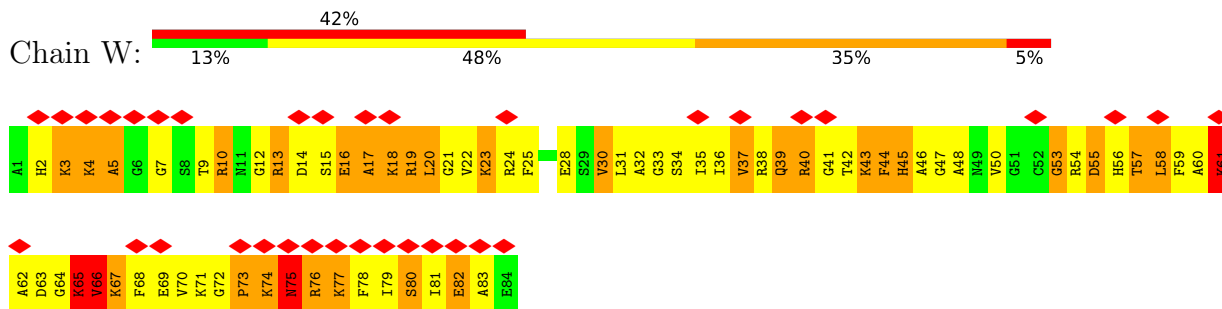
• Molecule 29: 50S ribosomal protein L24



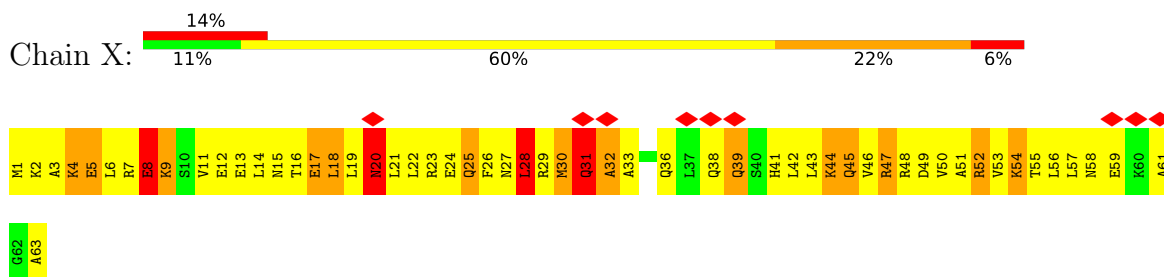
• Molecule 30: 50S ribosomal protein L25



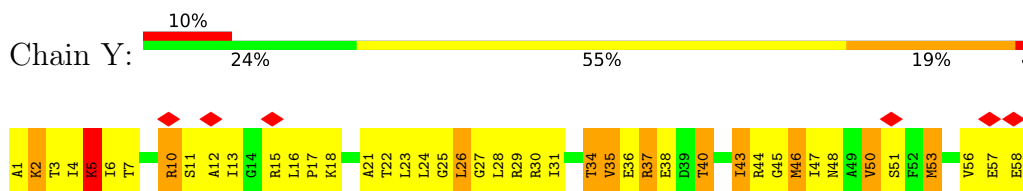
• Molecule 31: 50S ribosomal protein L27



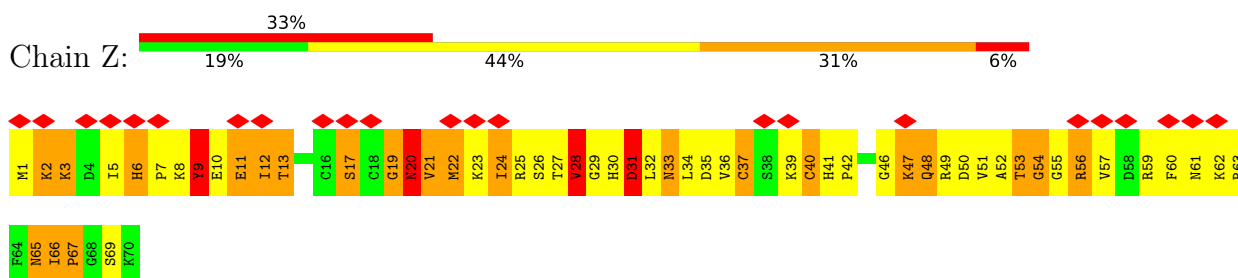
• Molecule 32: 50S ribosomal protein L29



• Molecule 33: 50S ribosomal protein L30



• Molecule 34: 50S ribosomal protein L31



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	Not provided	
Resolution determination method	FSC 0.5 CUT-OFF	Depositor
CTF correction method	Not provided	
Microscope	FEI TECNAI F30	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	Not provided	
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	KODAK SO-163 FILM	Depositor
Maximum map value	7.522	Depositor
Minimum map value	-4.419	Depositor
Average map value	0.037	Depositor
Map value standard deviation	0.632	Depositor
Recommended contour level	0.704	Depositor
Map size ( $\text{\AA}$ )	361.62, 361.62, 361.62	wwPDB
Map dimensions	294, 294, 294	wwPDB
Map angles ( $^\circ$ )	90, 90, 90	wwPDB
Pixel spacing ( $\text{\AA}$ )	1.23, 1.23, 1.23	Depositor

## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MG

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 5$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z  > 5$	RMSZ	# $ Z  > 5$
1	0	0.53	0/450	1.29	6/599 (1.0%)
2	1	0.40	0/448	0.92	1/594 (0.2%)
3	2	0.36	0/380	0.97	1/498 (0.2%)
4	3	0.49	0/513	1.06	2/676 (0.3%)
5	4	0.39	0/303	1.14	5/397 (1.3%)
6	7	0.69	0/153	1.12	1/207 (0.5%)
7	8	1.21	10/1775 (0.6%)	1.45	17/2755 (0.6%)
8	9	4.08	67/3329 (2.0%)	3.51	139/4446 (3.1%)
9	A	0.29	0/2803	0.66	1/4371 (0.0%)
10	B	0.31	7/68314 (0.0%)	0.67	102/106569 (0.1%)
11	C	0.51	0/2092	1.27	30/2813 (1.1%)
12	D	0.47	0/1586	1.15	18/2134 (0.8%)
13	E	0.81	4/1571 (0.3%)	1.07	7/2113 (0.3%)
14	F	0.59	1/1444 (0.1%)	1.51	35/1937 (1.8%)
15	G	0.36	0/1343	0.94	4/1816 (0.2%)
16	H	0.40	0/1122	0.99	6/1515 (0.4%)
17	I	0.79	5/1046 (0.5%)	1.18	13/1410 (0.9%)
18	J	0.39	0/1135	1.12	8/1529 (0.5%)
19	K	0.47	0/939	1.48	22/1258 (1.7%)
20	L	1.03	3/1062 (0.3%)	2.06	51/1413 (3.6%)
21	M	0.55	1/1093 (0.1%)	1.30	14/1460 (1.0%)
22	N	0.50	1/1021 (0.1%)	1.09	8/1364 (0.6%)
23	O	0.39	0/910	1.02	8/1219 (0.7%)
24	P	0.80	3/929 (0.3%)	1.97	43/1242 (3.5%)
25	Q	0.42	0/960	1.11	7/1278 (0.5%)
26	R	0.46	0/829	1.16	9/1107 (0.8%)
27	S	0.33	0/864	0.94	5/1156 (0.4%)
28	T	0.58	2/784 (0.3%)	1.08	7/1048 (0.7%)
29	U	0.47	0/787	1.44	18/1051 (1.7%)
30	V	0.30	0/766	0.77	1/1025 (0.1%)
31	W	0.47	0/642	1.10	5/848 (0.6%)
32	X	0.34	0/510	1.05	5/677 (0.7%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
33	Y	0.37	0/453	0.97	1/605 (0.2%)
34	Z	0.63	0/559	1.34	11/745 (1.5%)
All	All	0.84	104/102915 (0.1%)	1.04	611/153875 (0.4%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	0	0	1
7	8	0	1
8	9	1	15
9	A	0	1
10	B	1	65
11	C	0	2
24	P	0	1
26	R	0	1
34	Z	0	1
All	All	2	88

The worst 5 of 104 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	9	299	ASP	CB-CG	74.24	3.37	1.52
8	9	333	ASP	CB-CG	69.51	3.25	1.52
8	9	300	VAL	CB-CG1	68.35	3.78	1.52
8	9	319	LEU	C-N	-64.23	0.43	1.33
8	9	344	MET	C-N	-58.70	0.47	1.33

The worst 5 of 611 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	9	374	VAL	O-C-N	-113.18	8.76	121.94
8	9	299	ASP	CA-CB-CG	-82.38	30.22	112.60
8	9	370	ASP	CA-CB-CG	-53.17	59.43	112.60
8	9	333	ASP	CA-CB-CG	-44.91	67.69	112.60
8	9	319	LEU	O-C-N	-39.61	68.81	123.07

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
8	9	327	ASP	CA
10	B	2076	U	C3'

5 of 88 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	0	48	TYR	Sidechain
7	8	55	A	Sidechain
8	9	296	GLY	Peptide
8	9	299	ASP	Sidechain
8	9	319	LEU	Mainchain

## 5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	0	444	0	461	89	0
2	1	441	0	485	73	0
3	2	377	0	418	67	0
4	3	504	0	574	116	0
5	4	302	0	343	85	0
6	7	149	0	152	110	0
7	8	1590	0	808	80	0
8	9	3306	0	3403	1877	0
9	A	2507	0	1270	94	0
10	B	60995	0	30676	2402	0
11	C	2053	0	2122	435	0
12	D	1565	0	1616	324	0
13	E	1552	0	1619	283	0
14	F	1420	0	1460	183	0
15	G	1323	0	1374	165	0
16	H	1111	0	1148	155	0
17	I	1032	0	1088	222	0
18	J	1112	0	1147	237	0
19	K	930	0	1000	131	0
20	L	1053	0	1129	241	0
21	M	1074	0	1157	201	0
22	N	1008	0	1045	139	0

*Continued on next page...*

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
23	O	900	0	935	136	0
24	P	917	0	965	214	0
25	Q	947	0	1022	163	0
26	R	816	0	839	187	0
27	S	857	0	922	125	0
28	T	777	0	839	203	0
29	U	779	0	834	141	0
30	V	753	0	780	77	0
31	W	634	0	656	160	0
32	X	509	0	541	142	0
33	Y	449	0	491	68	0
34	Z	549	0	552	106	0
35	B	110	0	0	0	0
35	N	1	0	0	0	0
36	B	506	0	0	7	0
36	N	6	0	0	1	0
All	All	95358	0	63871	8357	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 53.

The worst 5 of 8357 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:9:410:VAL:CG1	10:B:485:C:H5''	1.27	1.65
8:9:145:ILE:CD1	8:9:161:PRO:HG2	1.17	1.64
8:9:334:PHE:CE2	8:9:420:PHE:HE2	1.02	1.63
8:9:2:PHE:CZ	8:9:295:LEU:HD13	1.31	1.62
8:9:334:PHE:CZ	8:9:420:PHE:CE2	1.87	1.62

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	0	54/56 (96%)	30 (56%)	15 (28%)	9 (17%)	0	2
2	1	52/54 (96%)	21 (40%)	22 (42%)	9 (17%)	0	2
3	2	44/46 (96%)	24 (54%)	12 (27%)	8 (18%)	0	2
4	3	62/64 (97%)	35 (56%)	17 (27%)	10 (16%)	0	2
5	4	36/38 (95%)	13 (36%)	11 (31%)	12 (33%)	0	0
6	7	16/18 (89%)	14 (88%)	2 (12%)	0	100	100
8	9	403/430 (94%)	154 (38%)	100 (25%)	149 (37%)	0	0
11	C	265/267 (99%)	97 (37%)	93 (35%)	75 (28%)	0	0
12	D	207/209 (99%)	96 (46%)	67 (32%)	44 (21%)	0	2
13	E	199/201 (99%)	87 (44%)	63 (32%)	49 (25%)	0	1
14	F	176/178 (99%)	92 (52%)	52 (30%)	32 (18%)	0	2
15	G	174/176 (99%)	117 (67%)	39 (22%)	18 (10%)	0	6
16	H	147/149 (99%)	84 (57%)	44 (30%)	19 (13%)	0	4
17	I	139/141 (99%)	123 (88%)	11 (8%)	5 (4%)	2	20
18	J	138/140 (99%)	70 (51%)	36 (26%)	32 (23%)	0	1
19	K	119/121 (98%)	72 (60%)	25 (21%)	22 (18%)	0	2
20	L	142/144 (99%)	66 (46%)	37 (26%)	39 (28%)	0	0
21	M	134/136 (98%)	79 (59%)	31 (23%)	24 (18%)	0	2
22	N	125/127 (98%)	82 (66%)	32 (26%)	11 (9%)	0	8
23	O	115/117 (98%)	64 (56%)	33 (29%)	18 (16%)	0	3
24	P	112/114 (98%)	42 (38%)	38 (34%)	32 (29%)	0	0
25	Q	115/117 (98%)	79 (69%)	22 (19%)	14 (12%)	0	4
26	R	101/103 (98%)	43 (43%)	30 (30%)	28 (28%)	0	0
27	S	108/110 (98%)	67 (62%)	20 (18%)	21 (19%)	0	2
28	T	97/99 (98%)	42 (43%)	33 (34%)	22 (23%)	0	1
29	U	100/102 (98%)	46 (46%)	41 (41%)	13 (13%)	0	4
30	V	92/94 (98%)	59 (64%)	27 (29%)	6 (6%)	1	12
31	W	82/84 (98%)	31 (38%)	29 (35%)	22 (27%)	0	0
32	X	61/63 (97%)	38 (62%)	15 (25%)	8 (13%)	0	4
33	Y	56/58 (97%)	35 (62%)	18 (32%)	3 (5%)	1	15

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
34	Z	68/70 (97%)	37 (54%)	22 (32%)	9 (13%)	0	4
All	All	3739/3826 (98%)	1939 (52%)	1037 (28%)	763 (20%)	0	2

5 of 763 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	0	31	LYS
1	0	35	GLU
1	0	45	ASP
2	1	12	SER
2	1	23	THR

### 5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	0	47/47 (100%)	30 (64%)	17 (36%)	0	1
2	1	48/48 (100%)	34 (71%)	14 (29%)	0	2
3	2	38/38 (100%)	29 (76%)	9 (24%)	1	4
4	3	51/51 (100%)	41 (80%)	10 (20%)	1	7
5	4	34/34 (100%)	21 (62%)	13 (38%)	0	1
6	7	16/17 (94%)	15 (94%)	1 (6%)	16	37
8	9	357/357 (100%)	325 (91%)	32 (9%)	9	27
11	C	213/213 (100%)	145 (68%)	68 (32%)	0	2
12	D	164/164 (100%)	112 (68%)	52 (32%)	0	2
13	E	165/165 (100%)	120 (73%)	45 (27%)	0	3
14	F	149/149 (100%)	116 (78%)	33 (22%)	1	6
15	G	137/137 (100%)	110 (80%)	27 (20%)	1	7
16	H	114/114 (100%)	86 (75%)	28 (25%)	1	4
17	I	109/109 (100%)	104 (95%)	5 (5%)	24	45
18	J	114/114 (100%)	85 (75%)	29 (25%)	0	3

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
19	K	102/102 (100%)	74 (72%)	28 (28%)	0	3
20	L	103/103 (100%)	63 (61%)	40 (39%)	0	1
21	M	109/109 (100%)	67 (62%)	42 (38%)	0	1
22	N	103/103 (100%)	78 (76%)	25 (24%)	1	4
23	O	87/87 (100%)	70 (80%)	17 (20%)	1	7
24	P	99/99 (100%)	65 (66%)	34 (34%)	0	1
25	Q	89/89 (100%)	69 (78%)	20 (22%)	1	6
26	R	84/84 (100%)	56 (67%)	28 (33%)	0	2
27	S	93/93 (100%)	77 (83%)	16 (17%)	2	9
28	T	83/83 (100%)	60 (72%)	23 (28%)	0	3
29	U	83/83 (100%)	57 (69%)	26 (31%)	0	2
30	V	78/78 (100%)	68 (87%)	10 (13%)	4	15
31	W	62/62 (100%)	44 (71%)	18 (29%)	0	2
32	X	55/55 (100%)	40 (73%)	15 (27%)	0	3
33	Y	48/48 (100%)	33 (69%)	15 (31%)	0	2
34	Z	62/62 (100%)	46 (74%)	16 (26%)	0	3
All	All	3096/3097 (100%)	2340 (76%)	756 (24%)	2	4

5 of 756 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
21	M	26	VAL
25	Q	16	ILE
21	M	81	ARG
21	M	22	GLN
23	O	18	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 97 such sidechains are listed below:

Mol	Chain	Res	Type
22	N	81	ASN
26	R	6	GLN
23	O	67	ASN
24	P	55	HIS
27	S	7	HIS

### 5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
10	B	2837/2904 (97%)	482 (16%)	22 (0%)
7	8	71/74 (95%)	4 (5%)	1 (1%)
9	A	116/117 (99%)	20 (17%)	1 (0%)
All	All	3024/3095 (97%)	506 (16%)	24 (0%)

5 of 506 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
7	8	39	A
7	8	77	C
7	8	85	A
7	8	89	A
9	A	13	G

5 of 24 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
10	B	1211	C
10	B	2198	A
10	B	2076	U
10	B	2282	G
10	B	199	A

## 5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

## 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 111 ligands modelled in this entry, 111 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
8	9	34
7	8	7

The worst 5 of 41 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	8	86:G	O3'	87:G	P	10.90
1	9	315:GLN	C	316:ALA	N	5.35
1	8	22:U	O3'	23:G	P	4.45
1	9	352:GLY	C	353:LYS	N	4.18
1	9	370:ASP	C	371:LYS	N	3.83

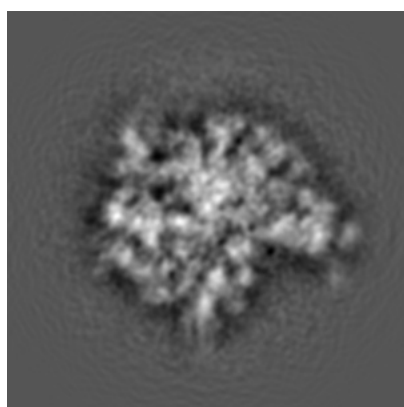
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-1261. These allow visual inspection of the internal detail of the map and identification of artifacts.

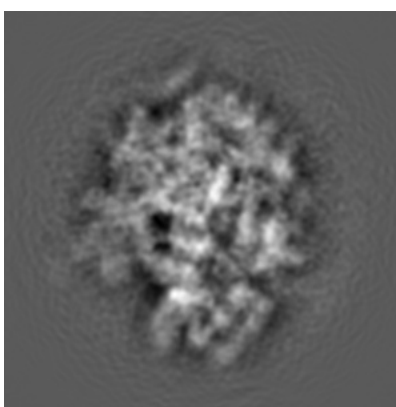
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

### 6.1 Orthogonal projections [i](#)

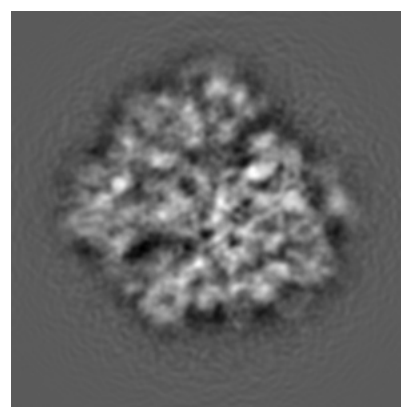
#### 6.1.1 Primary map



X



Y

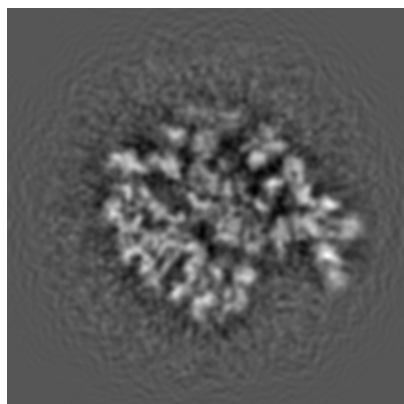


Z

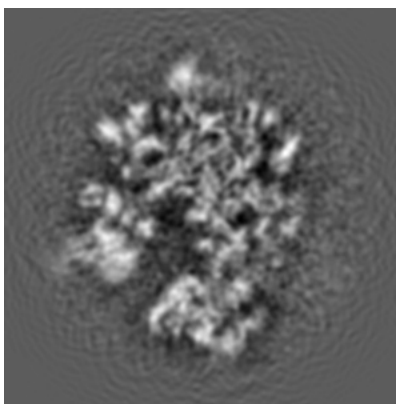
The images above show the map projected in three orthogonal directions.

### 6.2 Central slices [i](#)

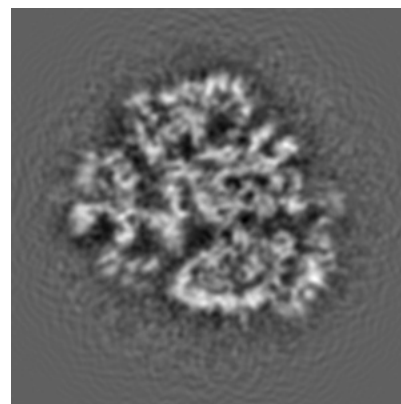
#### 6.2.1 Primary map



X Index: 147



Y Index: 147

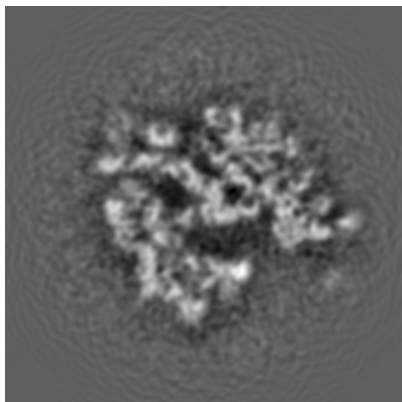


Z Index: 147

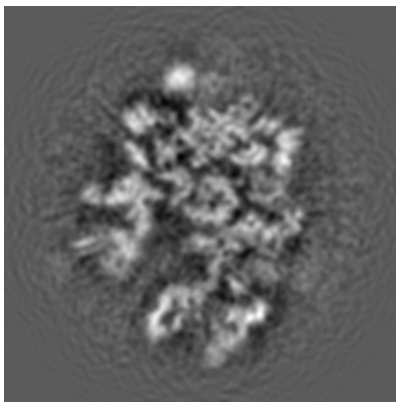
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [\(i\)](#)

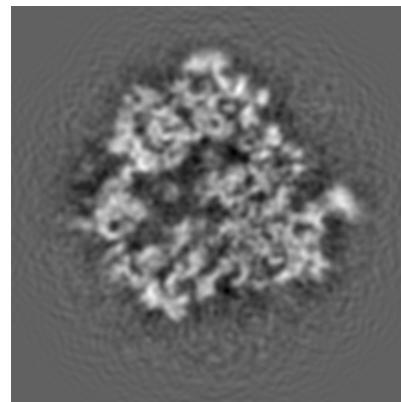
### 6.3.1 Primary map



X Index: 139



Y Index: 153

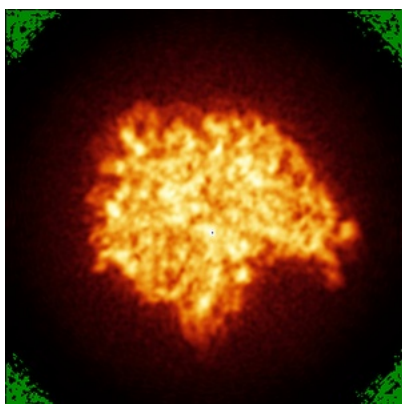


Z Index: 133

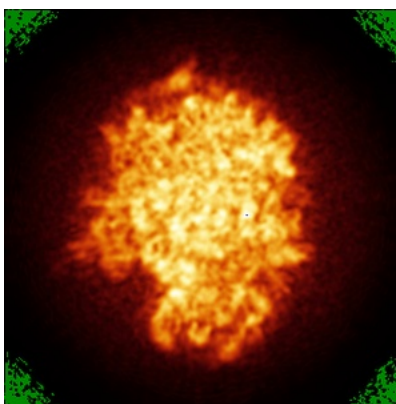
The images above show the largest variance slices of the map in three orthogonal directions.

## 6.4 Orthogonal standard-deviation projections (False-color) [\(i\)](#)

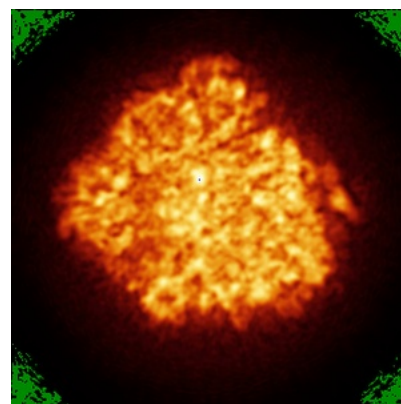
### 6.4.1 Primary map



X



Y

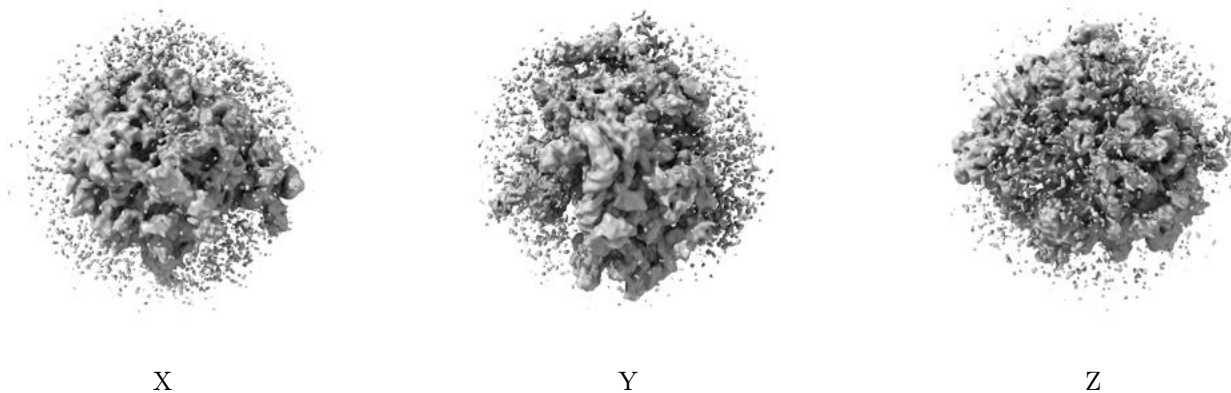


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.704. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

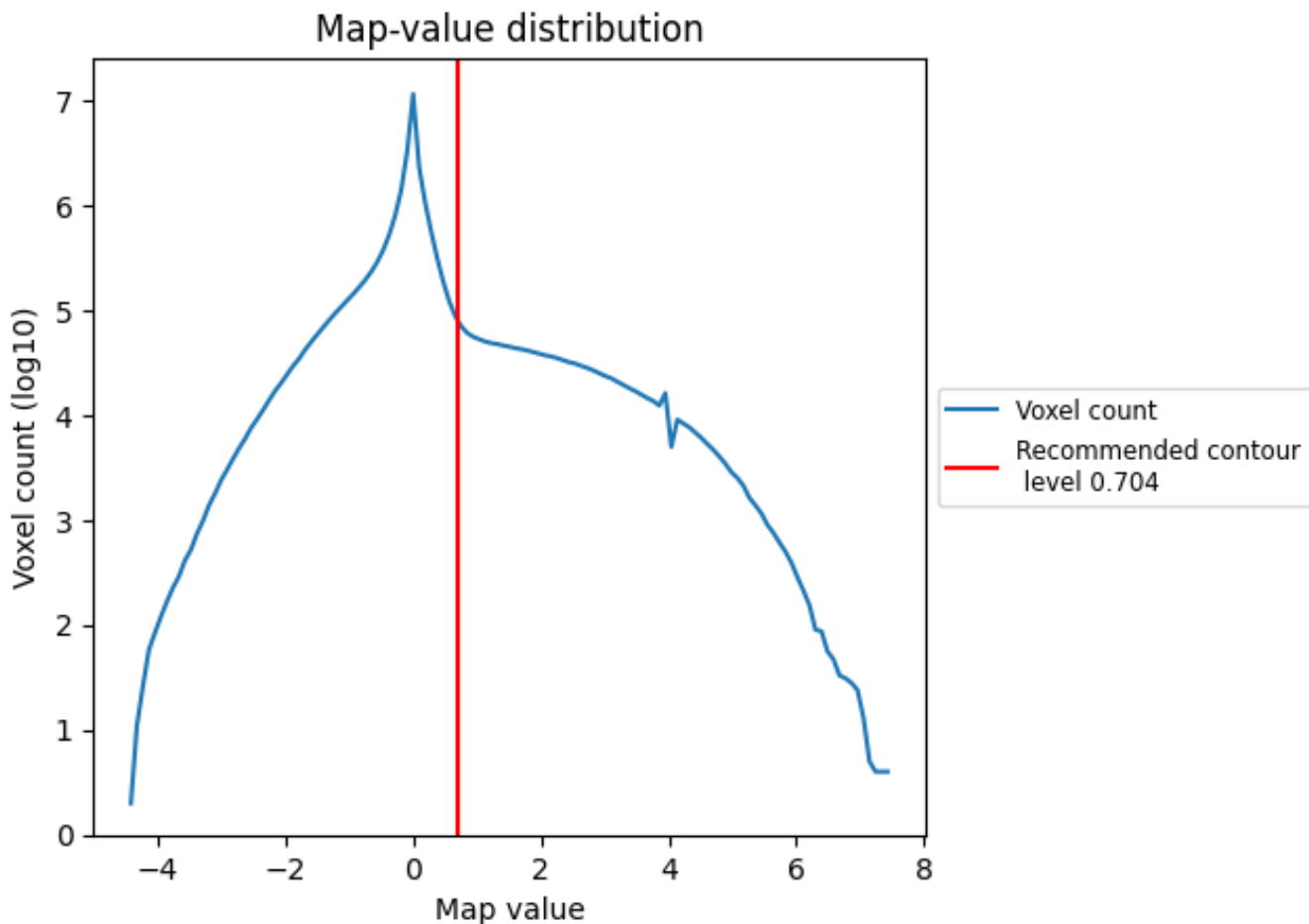
## 6.6 Mask visualisation [i](#)

This section was not generated. No masks/segmentation were deposited.

## 7 Map analysis [i](#)

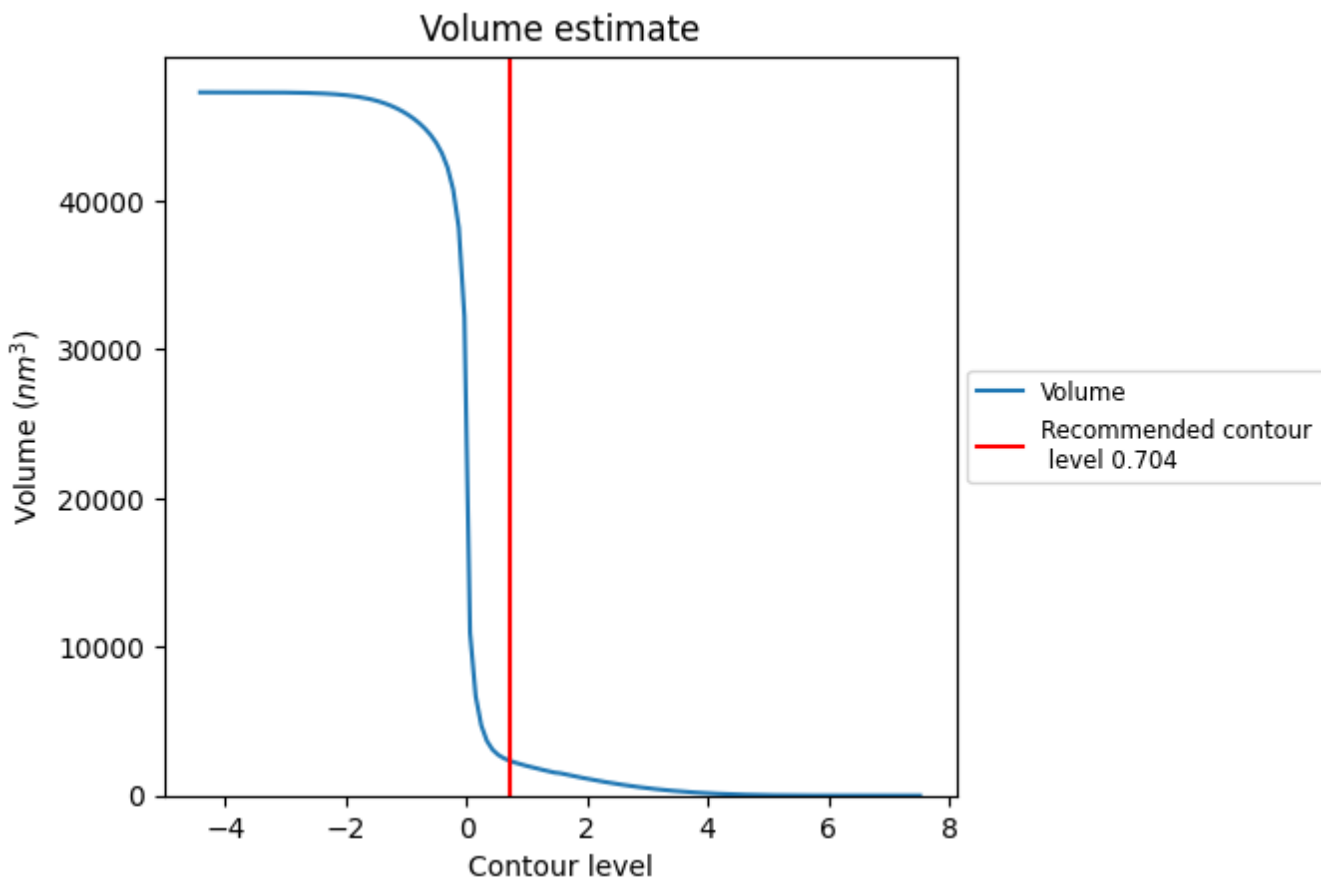
This section contains the results of statistical analysis of the map.

### 7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

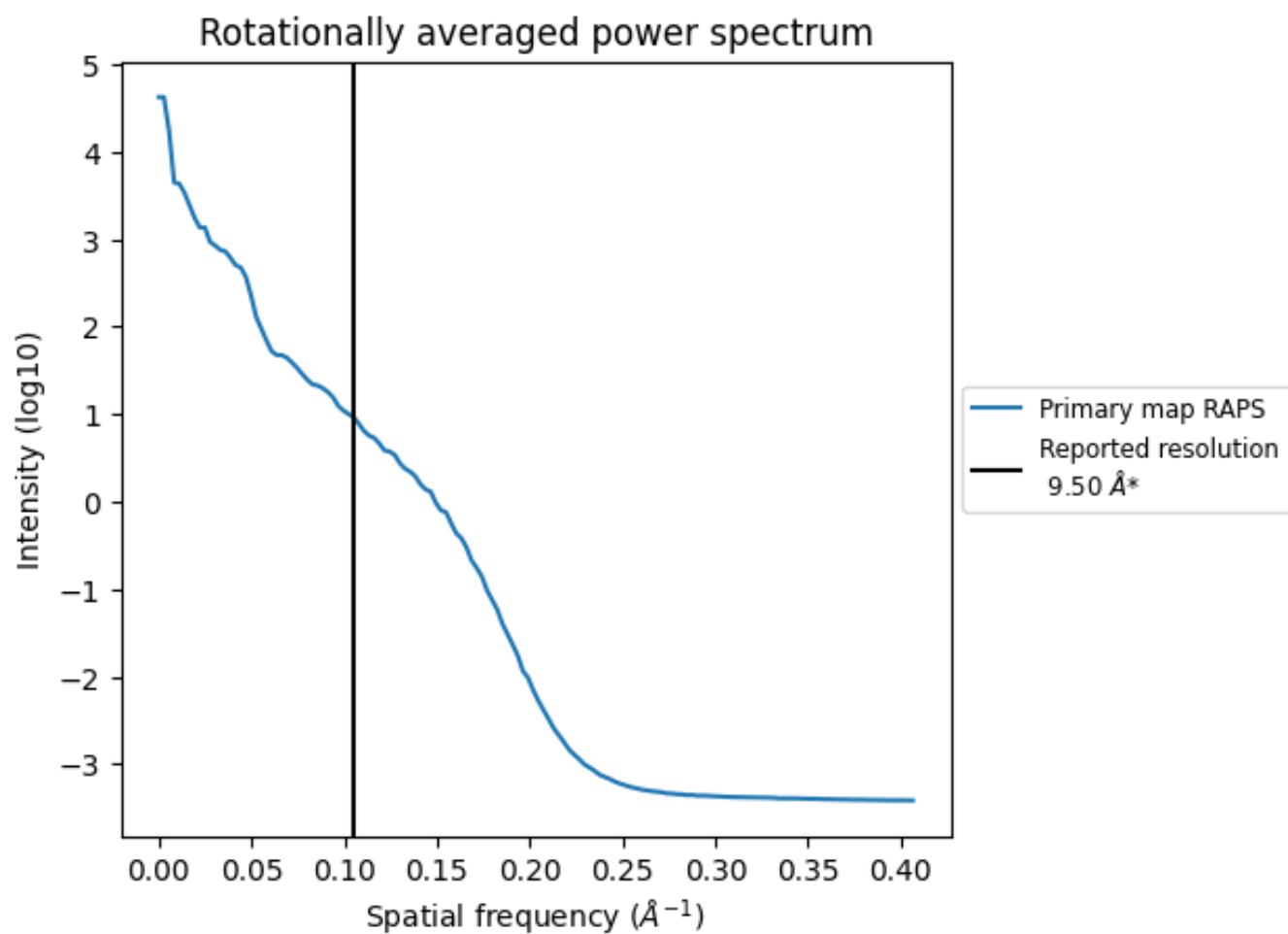
## 7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 2362 nm<sup>3</sup>; this corresponds to an approximate mass of 2133 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

### 7.3 Rotationally averaged power spectrum [i](#)



\*Reported resolution corresponds to spatial frequency of 0.105 Å<sup>-1</sup>

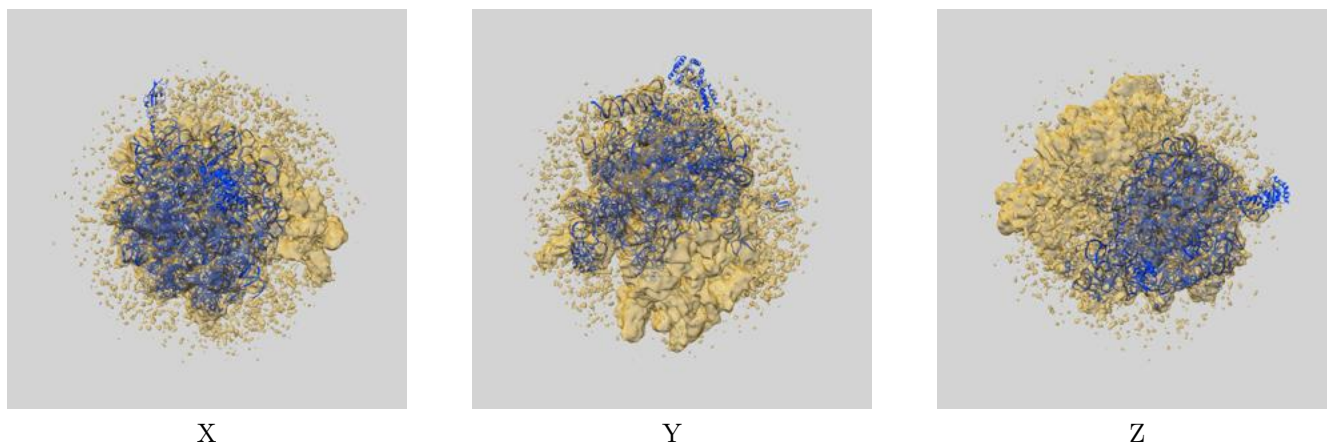
## 8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

## 9 Map-model fit [i](#)

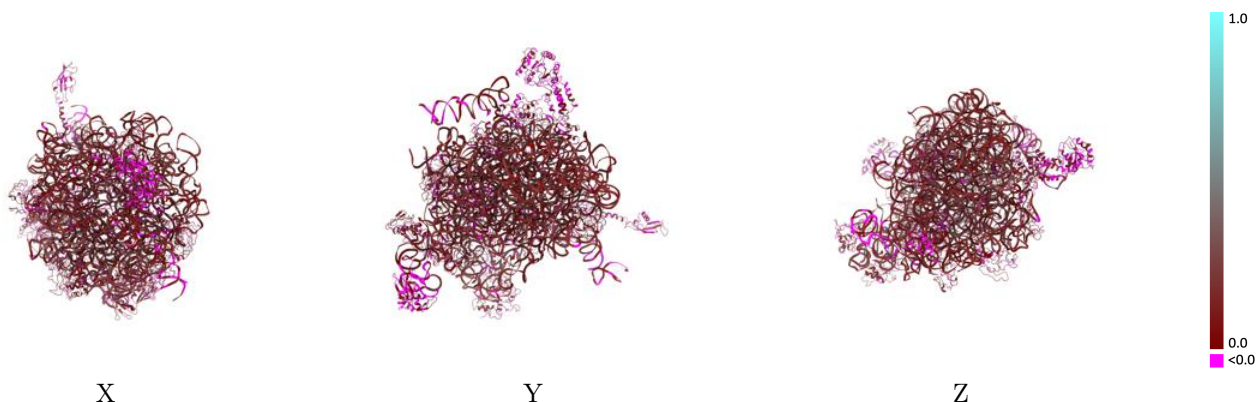
This section contains information regarding the fit between EMDB map EMD-1261 and PDB model 2J28. Per-residue inclusion information can be found in section 3 on page 11.

### 9.1 Map-model overlay [i](#)



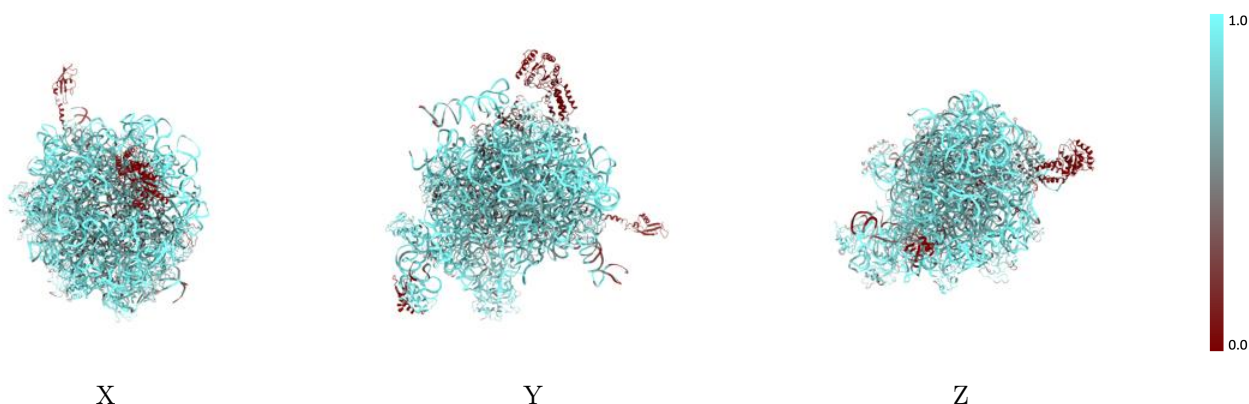
The images above show the 3D surface view of the map at the recommended contour level 0.704 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

## 9.2 Q-score mapped to coordinate model [i](#)



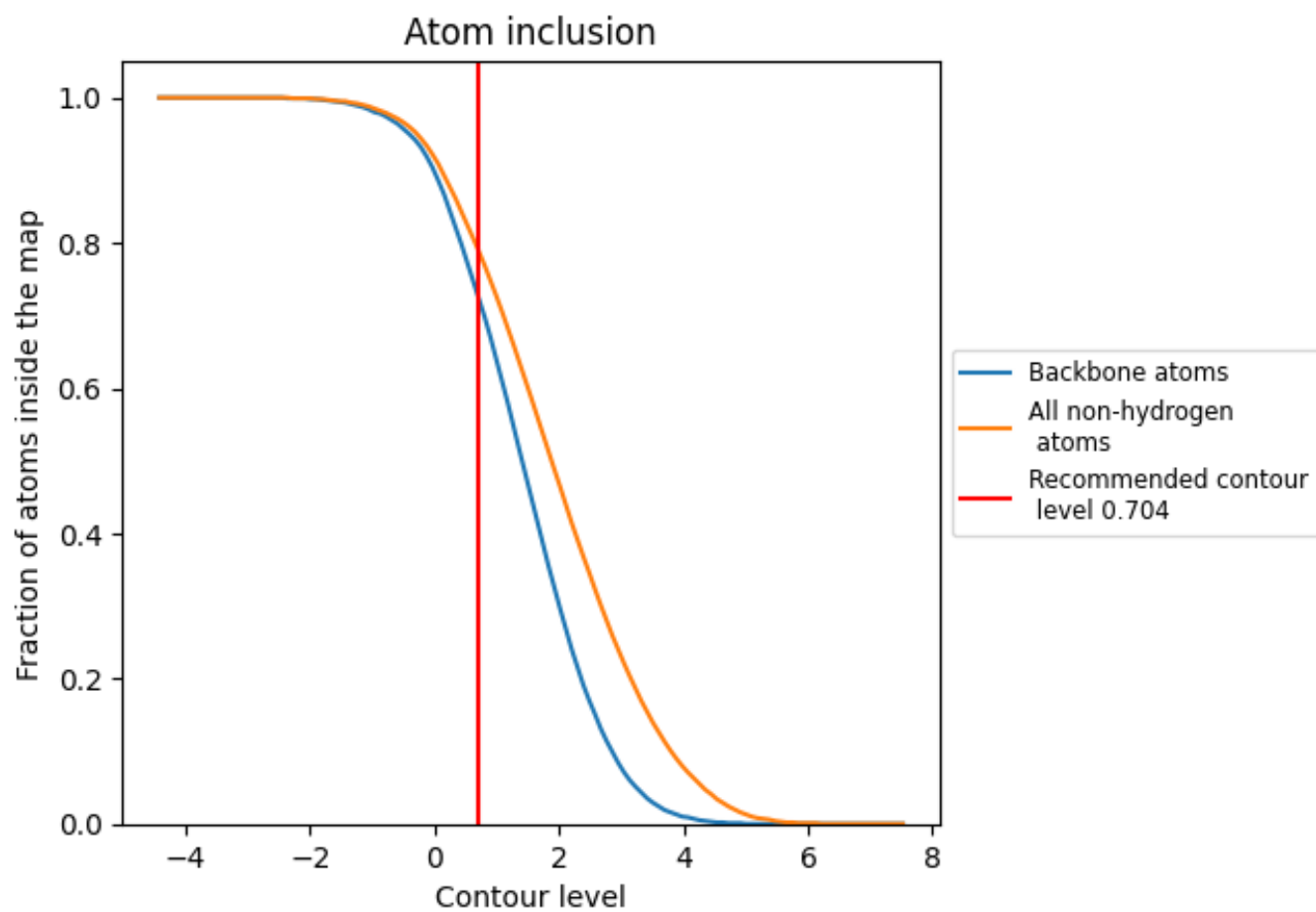
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

## 9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.704).







































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 73% of all backbone atoms, 79% of all non-hydrogen atoms, are inside the map.

## 9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.704) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7900	 0.1360
0	 0.5650	 0.1120
1	 0.5960	 0.0850
2	 0.4000	 0.0530
3	 0.4480	 0.0630
4	 0.4970	 0.0260
7	 0.5950	 0.0850
8	 0.8180	 0.0720
9	 0.2180	 0.0320
A	 0.9270	 0.1450
B	 0.8850	 0.1620
C	 0.5080	 0.0890
D	 0.6620	 0.1090
E	 0.6370	 0.0940
F	 0.8210	 0.0830
G	 0.8440	 0.1180
H	 0.2560	 0.0760
I	 0.5790	 0.0280
J	 0.6090	 0.1000
K	 0.6120	 0.1300
L	 0.5820	 0.0790
M	 0.5830	 0.0830
N	 0.6360	 0.1020
O	 0.7940	 0.0830
P	 0.6000	 0.1020
Q	 0.6560	 0.0990
R	 0.6910	 0.1060
S	 0.5800	 0.1180
T	 0.5930	 0.1040
U	 0.7260	 0.0880
V	 0.8860	 0.1160
W	 0.5240	 0.0560
X	 0.7280	 0.1110
Y	 0.7620	 0.1380
Z	 0.5910	 0.0890

